

SEQUENCE LISTING FREE TEXT

dgoA CDS for KDPGal Aldolase
dgoA CDS for KDPGal Aldolase
dgoA CDS for KDPGal Aldolase
aroB CDS for DHQ Synthase
tktA CDS for major Tranketolase isozyme
tktB CDS for minor Transketolase isozyme
Primer JWF 430
Primer JWF 449
Primer JWF 484
Primer JWF 529
Primer JWF 501
Primer JWF 499
Primer JWF 541
Primer JWF 542
Primer JWF 610
Primer JWF 611
Primer JWF 625
Primer JWF 626
Primer JWF 541
Primer JWF 542
Primer JWF 636
Primer JWF 637

Primer JWF 669

Primer JWF 670

Primer JWF 599

Primer JWF 560

Primer JWF 484

Primer JWF 529

IAP20 Receipt into 22 MAR 2006

SEQUENCE LISTING

<110> Board of Trustees operating Michigan State University
 Frost, John W.
 <120> Methods and Materials for the Production of Shikimic Acid
 <130> 6550-000086
 <150> US 60/505,658
 <151> 2003-09-24
 <160> 34
 <170> PatentIn version 3.3
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 <211> 618
 <212> DNA
 <213> Escherichia coli

<220>
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 <222> (1)...(615)
 <223> dgoA CDS for KDPGal Aldolase

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acg ccc gac gag gcg ctg gcg cat gtt ggc gcg gtg att gac gcc ggg 96
 Thr Pro Asp Glu Ala Leu Ala His Val Gly Ala Val Ile Asp Ala Gly
 20 25 30

ttc gac gcg gtt gaa atc ccg ctg aat tcc cca caa tgg gag caa agc 144
 Phe Asp Ala Val Glu Ile Pro Leu Asn Ser Pro Gln Trp Glu Gln Ser
 35 40 45

att ccc gcc atc gtt gat gcg tac ggc gac aag gcg ttg att ggc gca 192
 Ile Pro Ala Ile Val Asp Ala Tyr Gly Asp Lys Ala Leu Ile Gly Ala
 50 55 60

ggt acg gta ctg aaa cct gaa cag gtc gat gcg ctc gcc agg atg ggc 240
 Gly Thr Val Leu Lys Pro Glu Gln Val Asp Ala Leu Ala Arg Met Gly
 65 70 75 80

tgt cag ctc atc gtt acg ccc aat atc cat agt gaa gtg atc cgc cgt 288
 Cys Gln Leu Ile Val Thr Pro Asn Ile His Ser Glu Val Ile Arg Arg
 85 90 95

gcg gtg ggc tac ggc atg acc gtc tgc ccc ggc tgc gcg acg gcg acc 336
 Ala Val Gly Tyr Gly Met Thr Val Cys Pro Gly Cys Ala Thr Ala Thr
 100 105 110

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| gaa gcc ttt acc gcg ctc gaa gcg ggc gcg cag gcg ctg aaa ata ttt | 384 |
| Glu Ala Phe Thr Ala Leu Glu Ala Gly Ala Gln Ala Leu Lys Ile Phe | |
| 115 120 125 | |
| ccg tca tcg gct ttt ggt ccg caa tac atc aaa gcg tta aaa gcg gta | 432 |
| Pro Ser Ser Ala Phe Gly Pro Gln Tyr Ile Lys Ala Leu Lys Ala Val | |
| 130 135 140 | |
| ttg cca tcg gac atc gca gtc ttt gcc gtt ggc ggc gtg acg cca gaa | 480 |
| Leu Pro Ser Asp Ile Ala Val Phe Ala Val Gly Gly Val Thr Pro Glu | |
| 145 150 155 160 | |
| aac ctg gcg cag tgg ata gac gca ggt tgt gca ggg gcg ggc tta ggc | 528 |
| Asn Leu Ala Gln Trp Ile Asp Ala Gly Cys Ala Gly Ala Gly Leu Gly | |
| 165 170 175 | |
| agc gat ctc tat cgc gcc ggg caa tcc gta gag cgc acc gcg cag cag | 576 |
| Ser Asp Leu Tyr Arg Ala Gly Gln Ser Val Glu Arg Thr Ala Gln Gln | |
| 180 185 190 | |
| gca gca gca ttt gtt aag gcg tat cga gag gca gtg caa tga | 618 |
| Ala Ala Ala Phe Val Lys Ala Tyr Arg Glu Ala Val Gln | |
| 195 200 205 | |

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<212> PRT
<213> Escherichia coli

<400> 2

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Phe Asp Ala Val Glu Ile Pro Leu Asn Ser Pro Gln Trp Glu Gln Ser
35 40 45

Ile Pro Ala Ile Val Asp Ala Tyr Gly Asp Lys Ala Leu Ile Gly Ala
50 55 60

Gly Thr Val Leu Lys Pro Glu Gln Val Asp Ala Leu Ala Arg Met Gly
65 70 75 80

Cys Gln Leu Ile Val Thr Pro Asn Ile His Ser Glu Val Ile Arg Arg
85 90 95

Ala Val Gly Tyr Gly Met Thr Val Cys Pro Gly Cys Ala Thr Ala Thr
 100 105 110

Glu Ala Phe Thr Ala Leu Glu Ala Gly Ala Gln Ala Leu Lys Ile Phe
 115 120 125

Pro Ser Ser Ala Phe Gly Pro Gln Tyr Ile Lys Ala Leu Lys Ala Val
 130 135 140

Leu Pro Ser Asp Ile Ala Val Phe Ala Val Gly Gly Val Thr Pro Glu
 145 150 155 160

Asn Leu Ala Gln Trp Ile Asp Ala Gly Cys Ala Gly Ala Gly Leu Gly
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Ser Asp Leu Tyr Arg Ala Gly Gln Ser Val Glu Arg Thr Ala Gln Gln
 180 185 190

Ala Ala Ala Phe Val Lys Ala Tyr Arg Glu Ala Val Gln
 195 200 205

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 <212> DNA
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 <223> dgoA CDS for KDPGal Aldolase

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acg cca gac gag gcg ctg gct cac gtt ggc gcc gtt atc gac gcc ggt 96
 Thr Pro Asp Glu Ala Leu Ala His Val Gly Ala Val Ile Asp Ala Gly
 20 25 30

ttc gac gcg gtc gaa atc ccg ctg aac tcg ccg cag tgg gag aaa agt 144
 Phe Asp Ala Val Glu Ile Pro Leu Asn Ser Pro Gln Trp Glu Lys Ser
 35 40 45

att ccg cag gtc gac gct tac ggc gag cag gcg ctt atc ggc gcg 192
 Ile Pro Gln Val Val Asp Ala Tyr Gly Glu Gln Ala Leu Ile Gly Ala
 50 55 60

ggc acg gtg ctg caa ccg gag cag gtc gac agg ctg gcg gcc atg ggc 240

| | | | |
|---|-----|-----|-----|
| Gly Thr Val Leu Gln Pro Glu Gln Val Asp Arg Leu Ala Ala Met Gly | | | |
| 65 | 70 | 75 | 80 |
| tgt cgg ctg att gtg acg cca aac att caa ccg gaa gtg atc cgg cga | | | 288 |
| Cys Arg Leu Ile Val Thr Pro Asn Ile Gln Pro Glu Val Ile Arg Arg | | | |
| 85 | 90 | 95 | |
| gct gtg ggt tac ggc atg acc gtg tgt cca ggc tgc gcc acc gcc agc | | | 336 |
| Ala Val Gly Tyr Gly Met Thr Val Cys Pro Gly Cys Ala Thr Ala Ser | | | |
| 100 | 105 | 110 | |
| gaa gcc ttt agc gcg ctc gat gcc ggc gcg cag gcg cta aaa atc ttc | | | 384 |
| Glu Ala Phe Ser Ala Leu Asp Ala Gly Ala Gln Ala Leu Lys Ile Phe | | | |
| 115 | 120 | 125 | |
| ccg tca tcg gct ttt ggc ccg gat tac atc aaa gcg ttg aaa gcc gtg | | | 432 |
| Pro Ser Ser Ala Phe Gly Pro Asp Tyr Ile Lys Ala Leu Lys Ala Val | | | |
| 130 | 135 | 140 | |
| ctg ccg ccc gag gtt ccg gtc ttt gcc gtt ggc ggc gtg acg ccg gaa | | | 480 |
| Leu Pro Pro Glu Val Pro Val Phe Ala Val Gly Gly Val Thr Pro Glu | | | |
| 145 | 150 | 155 | 160 |
| aac ctg gcg cag tgg att aat gcc ggc tgt gtt ggg gca gga ttg ggt | | | 528 |
| Asn Leu Ala Gln Trp Ile Asn Ala Gly Cys Val Gly Ala Gly Leu Gly | | | |
| 165 | 170 | 175 | |
| agc gat ctc tat cgt gcc ggc cag tcg gtt gaa cgt acc gcg cag cag | | | 576 |
| Ser Asp Leu Tyr Arg Ala Gly Gln Ser Val Glu Arg Thr Ala Gln Gln | | | |
| 180 | 185 | 190 | |
| gca gcc gca ttc gta aaa gcg tat cga gag gca gtg aaa tga | | | 618 |
| Ala Ala Ala Phe Val Lys Ala Tyr Arg Glu Ala Val Lys | | | |
| 195 | 200 | 205 | |

<210> 4
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 <213> Klebsiella pneumoniae

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Phe Asp Ala Val Glu Ile Pro Leu Asn Ser Pro Gln Trp Glu Lys Ser
 35 40 45

Ile Pro Gln Val Val Asp Ala Tyr Gly Glu Gln Ala Leu Ile Gly Ala
 50 55 60

Gly Thr Val Leu Gln Pro Glu Gln Val Asp Arg Leu Ala Ala Met Gly
 65 70 75 80

Cys Arg Leu Ile Val Thr Pro Asn Ile Gln Pro Glu Val Ile Arg Arg
 85 90 95

Ala Val Gly Tyr Gly Met Thr Val Cys Pro Gly Cys Ala Thr Ala Ser
 100 105 110

Glu Ala Phe Ser Ala Leu Asp Ala Gly Ala Gln Ala Leu Lys Ile Phe
 115 120 125

Pro Ser Ser Ala Phe Gly Pro Asp Tyr Ile Lys Ala Leu Lys Ala Val
 130 135 140

Leu Pro Pro Glu Val Pro Val Phe Ala Val Gly Gly Val Thr Pro Glu
 145 150 155 160

Asn Leu Ala Gln Trp Ile Asn Ala Gly Cys Val Gly Ala Gly Leu Gly
 165 170 175

Ser Asp Leu Tyr Arg Ala Gly Gln Ser Val Glu Arg Thr Ala Gln Gln
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Ala Ala Ala Phe Val Lys Ala Tyr Arg Glu Ala Val Lys
 195 200 205

<210> 5
 <211> 618
 <212> DNA
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<220>
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 <222> (1)..(615)
 <223> *dgoA* CDS for KDPGal Aldolase

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 Met Gln Trp Gln Thr Asn Leu Pro Leu Ile Ala Ile Leu Arg Gly Ile
 1 5 10 15

acg ccc gat gat gcc ctg gcg cac gtt ggc gcg gtg gtg gat gcg gga 96
 Thr Pro Asp Asp Ala Leu Ala His Val Gly Ala Val Val Asp Ala Gly
 20 25 30

| | |
|---|-----|
| ttt gac gct ata gaa att ccg ctt aac tcc cca cag tgg gaa aaa agc Phe Asp Ala Ile Glu Ile Pro Leu Asn Ser Pro Gln Trp Glu Lys Ser 35 40 45 | 144 |
| att tct tcc gtg gtg aag gcg tat ggc ggc agg gcg ctt att ggc gct Ile Ser Ser Val Val Lys Ala Tyr Gly Gly Arg Ala Leu Ile Gly Ala 50 55 60 | 192 |
| ggt acc gta ctg aaa ccg gaa cag gta gac cag ctt gcc ggg atg ggc Gly Thr Val Leu Lys Pro Glu Gln Val Asp Gln Leu Ala Gly Met Gly 65 70 75 80 | 240 |
| tgc aag ctg atc gtc acg ccg aat atc caa ccg gag gtg atc cgc cgg Cys Lys Leu Ile Val Thr Pro Asn Ile Gln Pro Glu Val Ile Arg Arg 85 90 95 | 288 |
| gcg gtg agc tat ggc atg acc gtg tgt ccg ggc tgc gcc acg gca acg Ala Val Ser Tyr Gly Met Thr Val Cys Pro Gly Cys Ala Thr Ala Thr 100 105 110 | 336 |
| gaa gcc ttt tct gcg ctg gat gca ggc gca cag gcg tta aaa att ttc Glu Ala Phe Ser Ala Leu Asp Ala Gly Ala Gln Ala Leu Lys Ile Phe 115 120 125 | 384 |
| ccg tcg tcg gcg ttt ggt ccg ggc tac atc agc gcg ctg aaa gcg gta Pro Ser Ser Ala Phe Gly Pro Gly Tyr Ile Ser Ala Leu Lys Ala Val 130 135 140 | 432 |
| ctt ccg ccg gat gtt ccg cta ttt gcc gtc ggc ggc gtg acg ccg gaa Leu Pro Pro Asp Val Pro Leu Phe Ala Val Gly Gly Val Thr Pro Glu 145 150 155 160 | 480 |
| aac cta gcg caa tgg att aaa gca ggc tgt gtg ggc gcg gga ttg ggt Asn Leu Ala Gln Trp Ile Lys Ala Gly Cys Val Gly Ala Gly Leu Gly 165 170 175 | 528 |
| agc gat ctc tat cgc gcc ggg caa tcc gtt gaa cgc acc gcg cag cag Ser Asp Leu Tyr Arg Ala Gly Gln Ser Val Glu Arg Thr Ala Gln Gln 180 185 190 | 576 |
| gct gcg gca ttt gtt aat gcg tat cga gag gca gtg aaa tga Ala Ala Ala Phe Val Asn Ala Tyr Arg Glu Ala Val Lys 195 200 205 | 618 |

<210> 6
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 <212> PRT
 <213> *Salmonella typhimurium*
 <400> 6

Met Gln Trp Gln Thr Asn Leu Pro Leu Ile Ala Ile Leu Arg Gly Ile
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Thr Pro Asp Asp Ala Leu Ala His Val Gly Ala Val Val Asp Ala Gly
20 25 30

Phe Asp Ala Ile Glu Ile Pro Leu Asn Ser Pro Gln Trp Glu Lys Ser
35 40 45

Ile Ser Ser Val Val Lys Ala Tyr Gly Gly Arg Ala Leu Ile Gly Ala
50 55 60

Gly Thr Val Leu Lys Pro Glu Gln Val Asp Gln Leu Ala Gly Met Gly
65 70 75 80

Cys Lys Leu Ile Val Thr Pro Asn Ile Gln Pro Glu Val Ile Arg Arg
85 90 95

Ala Val Ser Tyr Gly Met Thr Val Cys Pro Gly Cys Ala Thr Ala Thr
100 105 110

Glu Ala Phe Ser Ala Leu Asp Ala Gly Ala Gln Ala Leu Lys Ile Phe
115 120 125

Pro Ser Ser Ala Phe Gly Pro Gly Tyr Ile Ser Ala Leu Lys Ala Val
130 135 140

Leu Pro Pro Asp Val Pro Leu Phe Ala Val Gly Gly Val Thr Pro Glu
145 150 155 160

Asn Leu Ala Gln Trp Ile Lys Ala Gly Cys Val Gly Ala Gly Leu Gly
165 170 175

Ser Asp Leu Tyr Arg Ala Gly Gln Ser Val Glu Arg Thr Ala Gln Gln
180 185 190

Ala Ala Ala Phe Val Asn Ala Tyr Arg Glu Ala Val Lys
195 200 205

<210> 7
<211> 1089
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<213> Escherichia coli

<220>
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<222> (1)..(1086)

<223> aroB CDS for DHQ Synthase

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| 1 5 10 15 | | | |
| atc gca tct ggt ttg ttt aat gaa cca gct tca ttc tta ccg ctg aaa | | | 96 |
| Ile Ala Ser Gly Leu Phe Asn Glu Pro Ala Ser Phe Leu Pro Leu Lys | | | |
| 20 25 30 | | | |
| tcg ggc gag cag gtc atg ttg gtc acc aac gaa acc ctg gct cct ctg | | | 144 |
| Ser Gly Glu Gln Val Met Leu Val Thr Asn Glu Thr Leu Ala Pro Leu | | | |
| 35 40 45 | | | |
| tat ctc gat aag gtc cgc ggc gta ctt gaa cag gcg ggt gtt aac gtc | | | 192 |
| Tyr Leu Asp Lys Val Arg Gly Val Leu Glu Gln Ala Gly Val Asn Val | | | |
| 50 55 60 | | | |
| gat agc gtt atc ctc cct gac ggc gag cag tat aaa agc ctg gct gta | | | 240 |
| Asp Ser Val Ile Leu Pro Asp Gly Glu Gln Tyr Lys Ser Leu Ala Val | | | |
| 65 70 75 80 | | | |
| ctc gat acc gtc ttt acg gcg ttg tta caa aaa ccg cat ggt cgc gat | | | 288 |
| Leu Asp Thr Val Phe Thr Ala Leu Leu Gln Lys Pro His Gly Arg Asp | | | |
| 85 90 95 | | | |
| act acg ctg gtg gcg ctt ggc ggc gta gtg ggc gat ctg acc ggc | | | 336 |
| Thr Thr Leu Val Ala Leu Gly Gly Val Val Gly Asp Leu Thr Gly | | | |
| 100 105 110 | | | |
| ttc gcg gcg agt tat cag cgc ggt gtc cgt ttc att caa gtc ccg | | | 384 |
| Phe Ala Ala Ala Ser Tyr Gln Arg Gly Val Arg Phe Ile Gln Val Pro | | | |
| 115 120 125 | | | |
| acg acg tta ctg tcg cag gtc gat tcc tcc gtt ggc ggc aaa act gcg | | | 432 |
| Thr Thr Leu Leu Ser Gln Val Asp Ser Ser Val Gly Gly Lys Thr Ala | | | |
| 130 135 140 | | | |
| gtc aac cat ccc ctc ggt aaa aac atg att ggc gcg ttc tac caa cct | | | 480 |
| Val Asn His Pro Leu Gly Lys Asn Met Ile Gly Ala Phe Tyr Gln Pro | | | |
| 145 150 155 160 | | | |
| gct tca gtg gtg gat ctc gac tgt ctg aaa acg ctt ccc ccg cgt | | | 528 |
| Ala Ser Val Val Val Asp Leu Asp Cys Leu Lys Thr Leu Pro Pro Arg | | | |
| 165 170 175 | | | |
| gag tta gcg tcg ggg ctg gca gaa gtc atc aaa tac ggc att att ctt | | | 576 |
| Glu Leu Ala Ser Gly Leu Ala Glu Val Ile Lys Tyr Gly Ile Ile Leu | | | |
| 180 185 190 | | | |
| gac ggt gcg ttt ttt aac tgg ctg gaa gag aat ctg gat gcg ttg ttg | | | 624 |
| Asp Gly Ala Phe Phe Asn Trp Leu Glu Glu Asn Leu Asp Ala Leu Leu | | | |
| 195 200 205 | | | |
| cgt ctg gac ggt ccg gca atg gcg tac tgt att cgc cgt tgt gaa | | | 672 |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| Arg | Leu | Asp | Gly | Pro | Ala | Met | Ala | Tyr | Cys | Ile | Arg | Arg | Cys | Cys | Glu | |
| 210 | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | 220 |
| ctg | aag | gca | gaa | gtt | gtc | gcc | gcc | gac | gag | cgc | gaa | acc | ggg | tta | cgt | 720 |
| Leu | Lys | Ala | Glu | Val | Val | Ala | Ala | Asp | Glu | Arg | Glu | Thr | Gly | Leu | Arg | |
| 225 | | | | | | | | | | | | | | | | 240 |
| | | | | | | | | | | | | | | | | |
| gct | tta | ctg | aat | ctg | gga | cac | acc | ttt | ggt | cat | gcc | att | gaa | gct | gaa | 768 |
| Ala | Leu | Leu | Asn | Leu | Gly | His | Thr | Phe | Gly | His | Ala | Ile | Glu | Ala | Glu | |
| 245 | | | | | | | | | | | | | | | | 255 |
| atg | ggg | tat | ggc | aat | tgg | tta | cat | ggt | gaa | gct | gtc | gct | gct | ggt | atg | 816 |
| Met | Gly | Tyr | Gly | Asn | Trp | Leu | His | Gly | Glu | Ala | Val | Ala | Ala | Gly | Met | |
| 260 | | | | | | | | | | | | | | | | 270 |
| gtg | atg | gct | gct | cg | ac | tc | gaa | cgt | ctc | gg | cag | ttt | agt | tct | gcc | 864 |
| Val | Met | Ala | Ala | Arg | Thr | Ser | Glu | Arg | Leu | Gly | Gln | Phe | Ser | Ser | Ala | |
| 275 | | | | | | | | | | | | | | | | 285 |
| gaa | ac | cag | cgt | att | ata | acc | ctg | ctc | aag | cg | gct | gg | tta | cc | gtc | 912 |
| Glu | Thr | Gln | Arg | Ile | Ile | Thr | Leu | Leu | Lys | Arg | Ala | Gly | Leu | Pro | Val | |
| 290 | | | | | | | | | | | | | | | | 300 |
| aat | ggg | cc | cg | gaa | atg | tcc | gc | cag | gc | tat | tta | cc | cat | atg | ctg | 960 |
| Asn | Gly | Pro | Arg | Glu | Met | Ser | Ala | Gln | Ala | Tyr | Leu | Pro | His | Met | Leu | |
| 305 | | | | | | | | | | | | | | | | 320 |
| cgt | gac | aag | aaa | gtc | ctt | gc | gga | gag | atg | cg | tta | att | ctt | cc | ttg | 1008 |
| Arg | Asp | Lys | Lys | Val | Leu | Ala | Gly | Glu | Met | Arg | Leu | Ile | Leu | Pro | Leu | |
| 325 | | | | | | | | | | | | | | | | 335 |
| gca | att | gg | aag | ag | gaa | gtt | cg | ac | gg | gtt | tc | ca | gag | ctt | gtt | 1056 |
| Ala | Ile | Gly | Lys | Ser | Glu | Val | Arg | Ser | Gly | Val | Ser | His | Glu | Leu | Val | |
| 340 | | | | | | | | | | | | | | | | 350 |
| ctt | aa | gc | att | gc | at | gc | at | tg | ca | tc | gc | ta | | | | 1089 |
| Leu | Asn | Ala | Ile | Ala | Asp | Cys | Gln | Ser | Ala | | | | | | | |
| 355 | | | | | | | | | | | | | | | | 360 |

<210> 8
 <211> 362
 <212> PRT
 <213> Escherichia coli

<400> 8

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Ser Gly Glu Gln Val Met Leu Val Thr Asn Glu Thr Leu Ala Pro Leu
 35 40 45

Tyr Leu Asp Lys Val Arg Gly Val Leu Glu Gln Ala Gly Val Asn Val
50 55 60

Asp Ser Val Ile Leu Pro Asp Gly Glu Gln Tyr Lys Ser Leu Ala Val
65 70 75 80

Leu Asp Thr Val Phe Thr Ala Leu Leu Gln Lys Pro His Gly Arg Asp
85 90 95

Thr Thr Leu Val Ala Leu Gly Gly Val Val Gly Asp Leu Thr Gly
100 105 110

Phe Ala Ala Ala Ser Tyr Gln Arg Gly Val Arg Phe Ile Gln Val Pro
115 120 125

Thr Thr Leu Leu Ser Gln Val Asp Ser Ser Val Gly Gly Lys Thr Ala
130 135 140

Val Asn His Pro Leu Gly Lys Asn Met Ile Gly Ala Phe Tyr Gln Pro
145 150 155 160

Ala Ser Val Val Val Asp Leu Asp Cys Leu Lys Thr Leu Pro Pro Arg
165 170 175

Glu Leu Ala Ser Gly Leu Ala Glu Val Ile Lys Tyr Gly Ile Ile Leu
180 185 190

Asp Gly Ala Phe Phe Asn Trp Leu Glu Glu Asn Leu Asp Ala Leu Leu
195 200 205

Arg Leu Asp Gly Pro Ala Met Ala Tyr Cys Ile Arg Arg Cys Cys Glu
210 215 220

Leu Lys Ala Glu Val Val Ala Ala Asp Glu Arg Glu Thr Gly Leu Arg
225 230 235 240

Ala Leu Leu Asn Leu Gly His Thr Phe Gly His Ala Ile Glu Ala Glu
245 250 255

Met Gly Tyr Gly Asn Trp Leu His Gly Glu Ala Val Ala Ala Gly Met
260 265 270

Val Met Ala Ala Arg Thr Ser Glu Arg Leu Gly Gln Phe Ser Ser Ala
 275 280 285

Glu Thr Gln Arg Ile Ile Thr Leu Leu Lys Arg Ala Gly Leu Pro Val
 290 295 300

Asn Gly Pro Arg Glu Met Ser Ala Gln Ala Tyr Leu Pro His Met Leu
 305 310 315 320

Arg Asp Lys Lys Val Leu Ala Gly Glu Met Arg Leu Ile Leu Pro Leu
 325 330 335

Ala Ile Gly Lys Ser Glu Val Arg Ser Gly Val Ser His Glu Leu Val
 340 345 350

Leu Asn Ala Ile Ala Asp Cys Gln Ser Ala
 355 360

<210> 9
 <211> 1992
 <212> DNA
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<220>
 <221> CDS
 <222> (1)..(1989)
 <223> tktA CDS for major Tranketolase isozyme

<400> 9
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 1 5 10 15

gac gca gta cag aaa gcc aaa tcc ggt cac ccg ggt gcc cct atg ggt 96
 Asp Ala Val Gln Lys Ala Lys Ser Gly His Pro Gly Ala Pro Met Gly
 20 25 30

atg gct gac att gcc gaa gtc ctg tgg cgt gat ttc ctg aaa cac aac 144
 Met Ala Asp Ile Ala Glu Val Leu Trp Arg Asp Phe Leu Lys His Asn
 35 40 45

ccg cag aat ccg tcc tgg gct gac cgt gac cgc ttc gtg ctg tcc aac 192
 Pro Gln Asn Pro Ser Trp Ala Asp Arg Asp Arg Phe Val Leu Ser Asn
 50 55 60

ggc cac ggc tcc atg ctg atc tac agc ctg ctg cac ctc acc ggt tac 240
 Gly His Gly Ser Met Leu Ile Tyr Ser Leu Leu His Leu Thr Gly Tyr
 65 70 75 80

| | |
|---|-----|
| gat ctg ccg atg gaa gaa ctg aaa aac ttc cgt cag ctg cac tct aaa | 288 |
| Asp Leu Pro Met Glu Glu Leu Lys Asn Phe Arg Gln Leu His Ser Lys | |
| 85 90 95 | |
| act ccg ggt cac ccg gaa gtt ggt tac acc gct ggt gtt gaa acc acc | 336 |
| Thr Pro Gly His Pro Glu Val Gly Tyr Thr Ala Gly Val Glu Thr Thr | |
| 100 105 110 | |
| acc ggt ccg ctg ggt cag ggt att gcc aac gca gtc ggt atg gcg att | 384 |
| Thr Gly Pro Leu Gly Gln Gly Ile Ala Asn Ala Val Gly Met Ala Ile | |
| 115 120 125 | |
| gca gaa aaa acg ctg gcg gcg cag ttt aac cgt ccg ggc cac gac att | 432 |
| Ala Glu Lys Thr Leu Ala Ala Gln Phe Asn Arg Pro Gly His Asp Ile | |
| 130 135 140 | |
| gtc gac cac tac acc tac gcc ttc atg ggc gac ggc tgc atg atg gaa | 480 |
| Val Asp His Tyr Thr Ala Phe Met Gly Asp Gly Cys Met Met Glu | |
| 145 150 155 160 | |
| ggc atc tcc cac gaa gtt tgc tct ctg gcg ggt acg ctg aag ctg ggt | 528 |
| Gly Ile Ser His Glu Val Cys Ser Leu Ala Gly Thr Leu Lys Leu Gly | |
| 165 170 175 | |
| aaa ctg att gca ttc tac gat gac aac ggt att tct atc gat ggt cac | 576 |
| Lys Leu Ile Ala Phe Tyr Asp Asp Asn Gly Ile Ser Ile Asp Gly His | |
| 180 185 190 | |
| gtt gaa ggc tgg ttc acc gac gac acc gca atg cgt ttc gaa gct tac | 624 |
| Val Glu Gly Trp Phe Thr Asp Asp Thr Ala Met Arg Phe Glu Ala Tyr | |
| 195 200 205 | |
| ggc tgg cac gtt att cgc gac atc gac ggt cat gac gcg gca tct atc | 672 |
| Gly Trp His Val Ile Arg Asp Ile Asp Gly His Asp Ala Ala Ser Ile | |
| 210 215 220 | |
| aaa cgc gca gta gaa gaa gcg cgc gca gtg act gac aaa cct tcc ctg | 720 |
| Lys Arg Ala Val Glu Ala Arg Ala Val Thr Asp Lys Pro Ser Leu | |
| 225 230 235 240 | |
| ctg atg tgc aaa acc atc atc ggt ttc ggt tcc ccg aac aaa gcc ggt | 768 |
| Leu Met Cys Lys Thr Ile Ile Gly Phe Gly Ser Pro Asn Lys Ala Gly | |
| 245 250 255 | |
| acc cac gac tcc cac ggt gcg ccg ctg ggc gac gct gaa att gcc ctg | 816 |
| Thr His Asp Ser His Gly Ala Pro Leu Gly Asp Ala Glu Ile Ala Leu | |
| 260 265 270 | |
| acc cgc gaa caa ctg ggc tgg aaa tat gcg ccg ttc gaa atc ccg tct | 864 |
| Thr Arg Glu Gln Leu Gly Trp Lys Tyr Ala Pro Phe Glu Ile Pro Ser | |
| 275 280 285 | |
| gaa atc tat gct cag tgg gat gcg aaa gaa gca ggc cag gcg aaa gaa | 912 |
| Glu Ile Tyr Ala Gln Trp Asp Ala Lys Glu Ala Gly Gln Ala Lys Glu | |
| 290 295 300 | |
| tcc gca tgg aac gag aaa ttc gct gct tac gcg aaa gct tat ccg cag | 960 |

| | | |
|---|------|--|
| Ser Ala Trp Asn Glu Lys Phe Ala Ala Tyr Ala Lys Ala Tyr Pro Gln | | |
| 305 310 315 320 | | |
| gaa gcc gct gaa ttt acc cgc cgt atg aaa ggc gaa atg ccg tct gac | 1008 | |
| Glu Ala Ala Glu Phe Thr Arg Arg Met Lys Gly Glu Met Pro Ser Asp | | |
| 325 330 335 | | |
| ttc gac gct aaa gcg aaa gag ttc atc gct aaa ctg cag gct aat ccg | 1056 | |
| Phe Asp Ala Lys Ala Lys Glu Phe Ile Ala Lys Leu Gln Ala Asn Pro | | |
| 340 345 350 | | |
| gcg aaa atc gcc agc cgt aaa gcg tct cag aat gct atc gaa gcg ttc | 1104 | |
| Ala Lys Ile Ala Ser Arg Lys Ala Ser Gln Asn Ala Ile Glu Ala Phe | | |
| 355 360 365 | | |
| ggc ccc ctg ttg ccg gaa ttc ctc ggc ggt tct gct gac ctg gcg ccg | 1152 | |
| Gly Pro Leu Leu Pro Glu Phe Leu Gly Gly Ser Ala Asp Leu Ala Pro | | |
| 370 375 380 | | |
| tct aac ctg acc ctg tgg tct ggt tct aaa gca atc aac gaa gat gct | 1200 | |
| Ser Asn Leu Thr Leu Trp Ser Gly Ser Lys Ala Ile Asn Glu Asp Ala | | |
| 385 390 395 400 | | |
| gcg ggt aac tac atc cac tac ggt gtt cgc gag ttc ggt atg acc gcg | 1248 | |
| Ala Gly Asn Tyr Ile His Tyr Gly Val Arg Glu Phe Gly Met Thr Ala | | |
| 405 410 415 | | |
| att gct aac ggt atc tcc ctg cac ggt ggc ttc ctg ccg tac acc tcc | 1296 | |
| Ile Ala Asn Gly Ile Ser Leu His Gly Gly Phe Leu Pro Tyr Thr Ser | | |
| 420 425 430 | | |
| acc ttc ctg atg ttc gtg gaa tac gca cgt aac gcc gta cgt atg gct | 1344 | |
| Thr Phe Leu Met Phe Val Glu Tyr Ala Arg Asn Ala Val Arg Met Ala | | |
| 435 440 445 | | |
| gcg ctg atg aaa cag cgt cag gtg atg gtt tac acc cac gac tcc atc | 1392 | |
| Ala Leu Met Lys Gln Arg Gln Val Met Val Tyr Thr His Asp Ser Ile | | |
| 450 455 460 | | |
| ggc ctg ggc gaa gac ggg ccg act cac cag ccg gtt gag cag gtc gct | 1440 | |
| Gly Leu Gly Glu Asp Gly Pro Thr His Gln Pro Val Glu Gln Val Ala | | |
| 465 470 475 480 | | |
| tct ctg cgc gta acc ccg aac atg tct aca tgg cgt ccg tgt gac cag | 1488 | |
| Ser Leu Arg Val Thr Pro Asn Met Ser Thr Trp Arg Pro Cys Asp Gln | | |
| 485 490 495 | | |
| gtt gaa tcc gcg gtc gcg tgg aaa tac ggt gtt gag cgt cag gac ggc | 1536 | |
| Val Glu Ser Ala Val Ala Trp Lys Tyr Gly Val Glu Arg Gln Asp Gly | | |
| 500 505 510 | | |
| ccg acc gca ctg atc ctc tcc cgt cag aac ctg gcg cag cag gaa cga | 1584 | |
| Pro Thr Ala Leu Ile Leu Ser Arg Gln Asn Leu Ala Gln Gln Glu Arg | | |
| 515 520 525 | | |
| act gaa gag caa ctg gca aac atc gcg cgc ggt ggt tat gtg ctg aaa | 1632 | |
| Thr Glu Glu Gln Leu Ala Asn Ile Ala Arg Gly Gly Tyr Val Leu Lys | | |

| 530 | 535 | 540 | |
|---|-----|-----|------|
| gac tgc gcc ggt cag ccg gaa ctg att ttc atc gct acc ggt tca gaa Asp Cys Ala Gly Gln Pro Glu Leu Ile Phe Ile Ala Thr Gly Ser Glu 545 550 555 560 | | | 1680 |
| gtt gaa ctg gct gtt gct gcc tac gaa aaa ctg act gcc gaa ggc gtg Val Glu Leu Ala Val Ala Ala Tyr Glu Lys Leu Thr Ala Glu Gly Val 565 570 575 | | | 1728 |
| aaa gcg cgc gtg gtg tcc atg tcg tct acc gac gca ttt gac aag cag Lys Ala Arg Val Val Ser Met Ser Ser Thr Asp Ala Phe Asp Lys Gln 580 585 590 | | | 1776 |
| gat gct gct tac cgt gaa tcc gta ctg ccg aaa gcg gtt act gca cgc Asp Ala Ala Tyr Arg Glu Ser Val Leu Pro Lys Ala Val Thr Ala Arg 595 600 605 | | | 1824 |
| gtt gct gta gaa gcg ggt att gct gac tac tgg tac aag tat gtt ggc Val Ala Val Glu Ala Gly Ile Ala Asp Tyr Trp Tyr Lys Tyr Val Gly 610 615 620 | | | 1872 |
| ctg aac ggt gct atc gtc ggt atg acc acc ttc ggt gaa tct gct ccg Leu Asn Gly Ala Ile Val Gly Met Thr Thr Phe Gly Glu Ser Ala Pro 625 630 635 640 | | | 1920 |
| gca gag ctg ttt gaa gag ttc ggc ttc act gtt gat aac gtt gtt Ala Glu Leu Leu Phe Glu Glu Phe Gly Phe Thr Val Asp Asn Val Val 645 650 655 | | | 1968 |
| gcg aaa gca aaa gaa ctg ctg taa Ala Lys Ala Lys Glu Leu Leu 660 | | | 1992 |

<210> 10
 <211> 663
 <212> PRT
 <213> Escherichia coli

<400> 10

Met Ser Ser Arg Lys Glu Leu Ala Asn Ala Ile Arg Ala Leu Ser Met
1 5 10 15

Asp Ala Val Gln Lys Ala Lys Ser Gly His Pro Gly Ala Pro Met Gly
20 25 30

Met Ala Asp Ile Ala Glu Val Leu Trp Arg Asp Phe Leu Lys His Asn
35 40 45

Pro Gln Asn Pro Ser Trp Ala Asp Arg Asp Arg Phe Val Leu Ser Asn
50 55 60

Gly His Gly Ser Met Leu Ile Tyr Ser Leu Leu His Leu Thr Gly Tyr
65 70 75 80

Asp Leu Pro Met Glu Glu Leu Lys Asn Phe Arg Gln Leu His Ser Lys
85 90 95

Thr Pro Gly His Pro Glu Val Gly Tyr Thr Ala Gly Val Glu Thr Thr
100 105 110

Thr Gly Pro Leu Gly Gln Gly Ile Ala Asn Ala Val Gly Met Ala Ile
115 120 125

Ala Glu Lys Thr Leu Ala Ala Gln Phe Asn Arg Pro Gly His Asp Ile
130 135 140

Val Asp His Tyr Thr Tyr Ala Phe Met Gly Asp Gly Cys Met Met Glu
145 150 155 160

Gly Ile Ser His Glu Val Cys Ser Leu Ala Gly Thr Leu Lys Leu Gly
165 170 175

Lys Leu Ile Ala Phe Tyr Asp Asp Asn Gly Ile Ser Ile Asp Gly His
180 185 190

Val Glu Gly Trp Phe Thr Asp Asp Thr Ala Met Arg Phe Glu Ala Tyr
195 200 205

Gly Trp His Val Ile Arg Asp Ile Asp Gly His Asp Ala Ala Ser Ile
210 215 220

Lys Arg Ala Val Glu Glu Ala Arg Ala Val Thr Asp Lys Pro Ser Leu
225 230 235 240

Leu Met Cys Lys Thr Ile Ile Gly Phe Gly Ser Pro Asn Lys Ala Gly
245 250 255

Thr His Asp Ser His Gly Ala Pro Leu Gly Asp Ala Glu Ile Ala Leu
260 265 270

Thr Arg Glu Gln Leu Gly Trp Lys Tyr Ala Pro Phe Glu Ile Pro Ser
275 280 285

Glu Ile Tyr Ala Gln Trp Asp Ala Lys Glu Ala Gly Gln Ala Lys Glu
290 295 300

Ser Ala Trp Asn Glu Lys Phe Ala Ala Tyr Ala Lys Ala Tyr Pro Gln
305 310 315 320

Glu Ala Ala Glu Phe Thr Arg Arg Met Lys Gly Glu Met Pro Ser Asp
325 330 335

Phe Asp Ala Lys Ala Lys Glu Phe Ile Ala Lys Leu Gln Ala Asn Pro
340 345 350

Ala Lys Ile Ala Ser Arg Lys Ala Ser Gln Asn Ala Ile Glu Ala Phe
355 360 365

Gly Pro Leu Leu Pro Glu Phe Leu Gly Gly Ser Ala Asp Leu Ala Pro
370 375 380

Ser Asn Leu Thr Leu Trp Ser Gly Ser Lys Ala Ile Asn Glu Asp Ala
385 390 395 400

Ala Gly Asn Tyr Ile His Tyr Gly Val Arg Glu Phe Gly Met Thr Ala
405 410 415

Ile Ala Asn Gly Ile Ser Leu His Gly Gly Phe Leu Pro Tyr Thr Ser
420 425 430

Thr Phe Leu Met Phe Val Glu Tyr Ala Arg Asn Ala Val Arg Met Ala
435 440 445

Ala Leu Met Lys Gln Arg Gln Val Met Val Tyr Thr His Asp Ser Ile
450 455 460

Gly Leu Gly Glu Asp Gly Pro Thr His Gln Pro Val Glu Gln Val Ala
465 470 475 480

Ser Leu Arg Val Thr Pro Asn Met Ser Thr Trp Arg Pro Cys Asp Gln
485 490 495

Val Glu Ser Ala Val Ala Trp Lys Tyr Gly Val Glu Arg Gln Asp Gly
500 505 510

Pro Thr Ala Leu Ile Leu Ser Arg Gln Asn Leu Ala Gln Gln Glu Arg

515

520

525

Thr Glu Glu Gln Leu Ala Asn Ile Ala Arg Gly Gly Tyr Val Leu Lys
 530 535 540

Asp Cys Ala Gly Gln Pro Glu Leu Ile Phe Ile Ala Thr Gly Ser Glu
 545 550 555 560

Val Glu Leu Ala Val Ala Ala Tyr Glu Lys Leu Thr Ala Glu Gly Val
 565 570 575

Lys Ala Arg Val Val Ser Met Ser Ser Thr Asp Ala Phe Asp Lys Gln
 580 585 590

Asp Ala Ala Tyr Arg Glu Ser Val Leu Pro Lys Ala Val Thr Ala Arg
 595 600 605

Val Ala Val Glu Ala Gly Ile Ala Asp Tyr Trp Tyr Lys Tyr Val Gly
 610 615 620

Leu Asn Gly Ala Ile Val Gly Met Thr Thr Phe Gly Glu Ser Ala Pro
 625 630 635 640

Ala Glu Leu Leu Phe Glu Glu Phe Gly Phe Thr Val Asp Asn Val Val
 645 650 655

Ala Lys Ala Lys Glu Leu Leu
 660

<210> 11
 <211> 2004
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)..(2001)
 <223> tktB CDS for minor Transketolase isozyme

<400> 11
 atg tcc cga aaa gac ctt gcc aat gcg att cgc gca ctc agt atg gat 48
 Met Ser Arg Lys Asp Leu Ala Asn Ala Ile Arg Ala Leu Ser Met Asp
 1 5 10 15

gcg gta caa aaa gcc aac tct ggt cat ccc ggc gcg ccg atg ggc atg 96
 Ala Val Gln Lys Ala Asn Ser Gly His Pro Gly Ala Pro Met Gly Met

| 20 | 25 | 30 | |
|--|-----|-----|-----|
| gct gat att gcc gaa gtg ctg tgg aac gat ttt ctt aaa cat aac cct Ala Asp Ile Ala Glu Val Leu Trp Asn Asp Phe Leu Lys His Asn Pro | | | 144 |
| 35 | 40 | 45 | |
| acc gac cca acc tgg tat gat cgc gac cgc ttt att ctt tcc aac ggt Thr Asp Pro Thr Trp Tyr Asp Arg Asp Arg Phe Ile Leu Ser Asn Gly | | | 192 |
| 50 | 55 | 60 | |
| cac gcg tcg atg ctg ctc tac agt ttg cta cat ctg acc ggt tac gac His Ala Ser Met Leu Leu Tyr Ser Leu Leu His Leu Thr Gly Tyr Asp | | | 240 |
| 65 | 70 | 75 | 80 |
| ctg ccg ctg gaa gaa ctg aag aac ttc cgt cag ttg cat tcg aaa acc Leu Pro Leu Glu Leu Lys Asn Phe Arg Gln Leu His Ser Lys Thr | | | 288 |
| 85 | 90 | 95 | |
| cca ggc cac ccg gag att ggc tat acg cca ggc gtt gaa acc acc acc Pro Gly His Pro Glu Ile Gly Tyr Thr Pro Gly Val Glu Thr Thr Thr | | | 336 |
| 100 | 105 | 110 | |
| ggc ccg ctt gga caa ggt ttg gcg aac gcc gtc ggg ctg gcg ata gca Gly Pro Leu Gly Gln Gly Leu Ala Asn Ala Val Gly Leu Ala Ile Ala | | | 384 |
| 115 | 120 | 125 | |
| gag cgt aca ctg gcg cag ttt aac cag cca gac cat gag atc gtc Glu Arg Thr Leu Ala Ala Gln Phe Asn Gln Pro Asp His Glu Ile Val | | | 432 |
| 130 | 135 | 140 | |
| gat cac ttc acc tat gtg ttt atg ggc gac ggc tgc ctg atg gaa ggt Asp His Phe Thr Tyr Val Phe Met Gly Asp Gly Cys Leu Met Glu Gly | | | 480 |
| 145 | 150 | 155 | 160 |
| att tcc cac gaa gtc tgt tcg ctg gca ggc acg ctg gga ctg ggc aag Ile Ser His Glu Val Cys Ser Leu Ala Gly Thr Leu Gly Leu Gly Lys | | | 528 |
| 165 | 170 | 175 | |
| ctg att ggt ttt tac gat cac aac ggt att tcc atc gac ggt gaa aca Leu Ile Gly Phe Tyr Asp His Asn Gly Ile Ser Ile Asp Gly Glu Thr | | | 576 |
| 180 | 185 | 190 | |
| gaa ggc tgg ttt acc gac gat acg gca aaa cgt ttt gaa gcc tat cac Glu Gly Trp Phe Thr Asp Asp Thr Ala Lys Arg Phe Glu Ala Tyr His | | | 624 |
| 195 | 200 | 205 | |
| tgg cat gtg atc cat gaa atc gac ggt cac gat ccg cag gcg gtg aag Trp His Val Ile His Glu Ile Asp Gly His Asp Pro Gln Ala Val Lys | | | 672 |
| 210 | 215 | 220 | |
| gaa gcg atc ctt gaa gcg caa agc gtg aaa gat aag ccg tcg ctg att Glu Ala Ile Leu Glu Ala Gln Ser Val Lys Asp Lys Pro Ser Leu Ile | | | 720 |
| 225 | 230 | 235 | 240 |
| atc tgc cgt acg gtg att ggc ttt ggt tcg ccg aat aaa gca ggt aag Ile Cys Arg Thr Val Ile Gly Phe Gly Ser Pro Asn Lys Ala Gly Lys | | | 768 |
| 245 | 250 | 255 | |

| | |
|---|------|
| gaa gag gcg cac ggc gca cca ctg ggg gaa gaa gaa gtg gcg ctg gca Glu Glu Ala His Gly Ala Pro Leu Gly Glu Glu Glu Val Ala Leu Ala 260 265 270 | 816 |
| cgg caa aaa ctg ggc tgg cac cat ccg cca ttt gag atc cct aaa gag Arg Gln Lys Leu Gly Trp His His Pro Pro Phe Glu Ile Pro Lys Glu 275 280 285 | 864 |
| att tat cac gcc tgg gat gcc cgt gaa aaa ggc gaa aaa gcg cag cag Ile Tyr His Ala Trp Asp Ala Arg Glu Lys Gly Glu Lys Ala Gln Gln 290 295 300 | 912 |
| agc tgg aat gag aag ttt gcc gcc tat aaa aag gct cat ccg caa ctg Ser Trp Asn Glu Lys Phe Ala Ala Tyr Lys Lys Ala His Pro Gln Leu 305 310 315 320 | 960 |
| gca gaa gag ttt acc cga cgg atg agc ggt ggt tta ccg aag gac tgg Ala Glu Glu Phe Thr Arg Arg Met Ser Gly Gly Leu Pro Lys Asp Trp 325 330 335 | 1008 |
| gag aaa acg act cag aaa tat atc aat gag tta cag gca aat ccg gcg Glu Lys Thr Thr Gln Lys Tyr Ile Asn Glu Leu Gln Ala Asn Pro Ala 340 345 350 | 1056 |
| aaa atc gct acc cgt aag gct tcg caa aat acg ctt aac gct tac ggg Lys Ile Ala Thr Arg Lys Ala Ser Gln Asn Thr Leu Asn Ala Tyr Gly 355 360 365 | 1104 |
| ccg atg ctg cct gag ttg ctc ggc ggt tcg gcg gat ctg gct ccc agc Pro Met Leu Pro Glu Leu Leu Gly Gly Ser Ala Asp Leu Ala Pro Ser 370 375 380 | 1152 |
| aac ctg acc atc tgg aaa ggt tct gtt tcg ctg aag gaa gat cca gcg Asn Leu Thr Ile Trp Lys Gly Ser Val Ser Leu Lys Glu Asp Pro Ala 385 390 395 400 | 1200 |
| ggc aac tac att cac tac ggg gtg cgt gaa ttt ggc atg acc gct atc Gly Asn Tyr Ile His Tyr Gly Val Arg Glu Phe Gly Met Thr Ala Ile 405 410 415 | 1248 |
| gcc aac ggc atc gcg cac cac ggc ttt gtg ccg tat acc gcg acg Ala Asn Gly Ile Ala His His Gly Gly Phe Val Pro Tyr Thr Ala Thr 420 425 430 | 1296 |
| ttc ctg atg ttt gtt gaa tac gcc cgt aac gcc gcg cgg atg gcg gca Phe Leu Met Phe Val Glu Tyr Ala Arg Asn Ala Ala Arg Met Ala Ala 435 440 445 | 1344 |
| ctg atg aaa gcg cgg cag att atg gtt tat acc cac gac tca att ggc Leu Met Lys Ala Arg Gln Ile Met Val Tyr Thr His Asp Ser Ile Gly 450 455 460 | 1392 |
| ctg ggc gaa gat ggt ccg acg cac cag gct gtt gag caa ctg gcc agc Leu Gly Glu Asp Gly Pro Thr His Gln Ala Val Glu Gln Leu Ala Ser 465 470 475 480 | 1440 |

| | |
|---|------|
| ctg cgc tta acg cca aat ttc agc acc tgg cga ccg tgc gat cag gtg Leu Arg Leu Thr Pro Asn Phe Ser Thr Trp Arg Pro Cys Asp Gln Val 485 490 495 | 1488 |
| gaa gcg gcg gtg ggc tgg aag ctg gcg gtt gag cgc cac aac gga ccg Glu Ala Ala Val Gly Trp Lys Leu Ala Val Glu Arg His Asn Gly Pro 500 505 510 | 1536 |
| acg gca ctg atc ctc tca agg cag aat ctg gcc cag gtg gaa cgt acg Thr Ala Leu Ile Leu Ser Arg Gln Asn Leu Ala Gln Val Glu Arg Thr 515 520 525 | 1584 |
| ccg gat cag gtt aaa gag att gct cgt ggc ggt tat gtg ctg aaa gac Pro Asp Gln Val Lys Glu Ile Ala Arg Gly Gly Tyr Val Leu Lys Asp 530 535 540 | 1632 |
| agc ggc ggt aag cca gat att att ctg att gcc acc ggt tca gag atg Ser Gly Gly Lys Pro Asp Ile Ile Leu Ile Ala Thr Gly Ser Glu Met 545 550 555 560 | 1680 |
| gaa att acc ctg caa gcg gca gag aaa tta gca gga gaa ggt cgc aat Glu Ile Thr Leu Gln Ala Ala Glu Lys Leu Ala Gly Glu Gly Arg Asn 565 570 575 | 1728 |
| gta cgc gta gtt tcc ctg ccc tcg acc gat att ttc gac gcc cag gat Val Arg Val Val Ser Leu Pro Ser Thr Asp Ile Phe Asp Ala Gln Asp 580 585 590 | 1776 |
| gag gaa tat cgg gag tcg gtg ttg cct tct aac gtt gct gcg gtc cgc gtg Glu Glu Tyr Arg Glu Ser Val Leu Pro Ser Asn Val Ala Ala Arg Val 595 600 605 | 1824 |
| gcg gtg gaa gca ggt att gcc gat tac tgg tac aag tat gtt ggt ctg Ala Val Glu Ala Gly Ile Ala Asp Tyr Trp Tyr Lys Tyr Val Gly Leu 610 615 620 | 1872 |
| aaa ggg gca att gtc ggg atg acg ggt tac ggg gaa tct gct ccg gcg Lys Gly Ala Ile Val Gly Met Thr Gly Tyr Gly Glu Ser Ala Pro Ala 625 630 635 640 | 1920 |
| gat aag ctg ttc ccg ttc ttt ggc ttt acc gcc gag aat att gtg gca Asp Lys Leu Phe Pro Phe Gly Phe Thr Ala Glu Asn Ile Val Ala 645 650 655 | 1968 |
| aaa gcg cat aag gtg ctg gga gtg aaa ggt gcc tga Lys Ala His Lys Val Leu Gly Val Lys Gly Ala 660 665 | 2004 |

<210> 12
 <211> 667
 <212> PRT
 <213> Escherichia coli
 <400> 12

Met Ser Arg Lys Asp Leu Ala Asn Ala Ile Arg Ala Leu Ser Met Asp

1

5

10

15

Ala Val Gln Lys Ala Asn Ser Gly His Pro Gly Ala Pro Met Gly Met
20 25 30

Ala Asp Ile Ala Glu Val Leu Trp Asn Asp Phe Leu Lys His Asn Pro
35 40 45

Thr Asp Pro Thr Trp Tyr Asp Arg Asp Arg Phe Ile Leu Ser Asn Gly
50 55 60

His Ala Ser Met Leu Leu Tyr Ser Leu Leu His Leu Thr Gly Tyr Asp
65 70 75 80

Leu Pro Leu Glu Glu Leu Lys Asn Phe Arg Gln Leu His Ser Lys Thr
85 90 95

Pro Gly His Pro Glu Ile Gly Tyr Thr Pro Gly Val Glu Thr Thr Thr
100 105 110

Gly Pro Leu Gly Gln Gly Leu Ala Asn Ala Val Gly Leu Ala Ile Ala
115 120 125

Glu Arg Thr Leu Ala Ala Gln Phe Asn Gln Pro Asp His Glu Ile Val
130 135 140

Asp His Phe Thr Tyr Val Phe Met Gly Asp Gly Cys Leu Met Glu Gly
145 150 155 160

Ile Ser His Glu Val Cys Ser Leu Ala Gly Thr Leu Gly Leu Gly Lys
165 170 175

Leu Ile Gly Phe Tyr Asp His Asn Gly Ile Ser Ile Asp Gly Glu Thr
180 185 190

Glu Gly Trp Phe Thr Asp Asp Thr Ala Lys Arg Phe Glu Ala Tyr His
195 200 205

Trp His Val Ile His Glu Ile Asp Gly His Asp Pro Gln Ala Val Lys
210 215 220

Glu Ala Ile Leu Glu Ala Gln Ser Val Lys Asp Lys Pro Ser Leu Ile

225 230 235 240

Ile Cys Arg Thr Val Ile Gly Phe Gly Ser Pro Asn Lys Ala Gly Lys
245 250 255

Glu Glu Ala His Gly Ala Pro Leu Gly Glu Glu Glu Val Ala Leu Ala
260 265 270

Arg Gln Lys Leu Gly Trp His His Pro Pro Phe Glu Ile Pro Lys Glu
275 280 285

Ile Tyr His Ala Trp Asp Ala Arg Glu Lys Gly Glu Lys Ala Gln Gln
290 295 300

Ser Trp Asn Glu Lys Phe Ala Ala Tyr Lys Lys Ala His Pro Gln Leu
305 310 315 320

Ala Glu Glu Phe Thr Arg Arg Met Ser Gly Gly Leu Pro Lys Asp Trp
325 330 335

Glu Lys Thr Thr Gln Lys Tyr Ile Asn Glu Leu Gln Ala Asn Pro Ala
340 345 350

Lys Ile Ala Thr Arg Lys Ala Ser Gln Asn Thr Leu Asn Ala Tyr Gly
355 360 365

Pro Met Leu Pro Glu Leu Leu Gly Gly Ser Ala Asp Leu Ala Pro Ser
370 375 380

Asn Leu Thr Ile Trp Lys Gly Ser Val Ser Leu Lys Glu Asp Pro Ala
385 390 395 400

Gly Asn Tyr Ile His Tyr Gly Val Arg Glu Phe Gly Met Thr Ala Ile
405 410 415

Ala Asn Gly Ile Ala His His Gly Gly Phe Val Pro Tyr Thr Ala Thr
420 425 430

Phe Leu Met Phe Val Glu Tyr Ala Arg Asn Ala Ala Arg Met Ala Ala
435 440 445

Leu Met Lys Ala Arg Gln Ile Met Val Tyr Thr His Asp Ser Ile Gly
450 455 460

Leu Gly Glu Asp Gly Pro Thr His Gln Ala Val Glu Gln Leu Ala Ser
465 470 475 480

Leu Arg Leu Thr Pro Asn Phe Ser Thr Trp Arg Pro Cys Asp Gln Val
485 490 495

Glu Ala Ala Val Gly Trp Lys Leu Ala Val Glu Arg His Asn Gly Pro
500 505 510

Thr Ala Leu Ile Leu Ser Arg Gln Asn Leu Ala Gln Val Glu Arg Thr
515 520 525

Pro Asp Gln Val Lys Glu Ile Ala Arg Gly Gly Tyr Val Leu Lys Asp
530 535 540

Ser Gly Gly Lys Pro Asp Ile Ile Leu Ile Ala Thr Gly Ser Glu Met
545 550 555 560

Glu Ile Thr Leu Gln Ala Ala Glu Lys Leu Ala Gly Glu Gly Arg Asn
565 570 575

Val Arg Val Val Ser Leu Pro Ser Thr Asp Ile Phe Asp Ala Gln Asp
580 585 590

Glu Glu Tyr Arg Glu Ser Val Leu Pro Ser Asn Val Ala Ala Arg Val
595 600 605

Ala Val Glu Ala Gly Ile Ala Asp Tyr Trp Tyr Lys Tyr Val Gly Leu
610 615 620

Lys Gly Ala Ile Val Gly Met Thr Gly Tyr Gly Glu Ser Ala Pro Ala
625 630 635 640

Asp Lys Leu Phe Pro Phe Phe Gly Phe Thr Ala Glu Asn Ile Val Ala
645 650 655

Lys Ala His Lys Val Leu Gly Val Lys Gly Ala
660 665

<210> 13

<211> 27

<212> DNA

<213> Artificial

<220>

<223> Primer JWF 430

<400> 13

gctctagatg cagtggcaaa ctaaact

27

<210> 14

<211> 29

<212> DNA

<213> Artificial

<220>

<223> Primer JWF 449

<400> 14

tagctctccg tcacgttact agatctcag

29

<210> 15

<211> 29

<212> DNA

<213> Artificial

<220>

<223> Primer JWF 484

<400> 15

gacggatcct ataaggagca tcgctcatg

29

<210> 16

<211> 30

<212> DNA

<213> Artificial

<220>

<223> Primer JWF 529

<400> 16

tagctctccg tcacgttact gacgtcgaag

30

<210> 17

<211> 20

<212> DNA

<213> Artificial

<220>

<223> Primer JWF 501

<400> 17

gacaggaata aggagcatcg

20

<210> 18
<211> 20
<212> DNA
<213> Artificial

<220>
<223> Primer JWF 499

<400> 18
ggaggtaaac ggtacgtgg 20

<210> 19
<211> 28
<212> DNA
<213> Artificial

<220>
<223> Primer JWF 541

<400> 19
ggaattcgca taaacaggat cgccatca 28

<210> 20
<211> 26
<212> DNA
<213> Artificial

<220>
<223> Primer JWF 542

<400> 20
ctggatcctt aagccacgct agccgt 26

<210> 21
<211> 29
<212> DNA
<213> Artificial

<220>
<223> Primer JWF 610

<400> 21
gtggatcctt aatccgttca tagtgtaaa 29

<210> 22
<211> 27
<212> DNA
<213> Artificial

<220>
<223> Primer JWF 611

<400> 22
tgggatccat gagaaaagccg actgcaa

27

<210> 23
<211> 20
<212> DNA
<213> Artificial

<220>
<223> Primer JWF 625

<400> 23
gttcgtcagt gcaggatgga

20

<210> 24
<211> 22
<212> DNA
<213> Artificial

<220>
<223> Primer JWF 626

<400> 24
gttcaggcgt gagtttctg ct

22

<210> 25
<211> 28
<212> DNA
<213> Artificial

<220>
<223> Primer JWF 541

<400> 25
ggaattcgca taaacaggat cgccatca

28

<210> 26
<211> 26
<212> DNA
<213> Artificial

<220>
<223> Primer JWF 542

<400> 26
ctggatcctt aagccacgcg agccgt

26

<210> 27
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Primer JWF 636

<400> 27
tccgtactgc gcgtatttag a

21

<210> 28
<211> 20
<212> DNA
<213> Artificial

<220>
<223> Primer JWF 637

<400> 28
agaggcgagt ttttcgacca

20

<210> 29
<211> 20
<212> DNA
<213> Artificial

<220>
<223> Primer JWF 669

<400> 29
gcagcattgt gccgccagaa

20

<210> 30
<211> 20
<212> DNA
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